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## Predicting the human epigenome from DNA motifs.

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### Public Summary:

The epigenome is established and maintained by the site-specific recruitment of chromatin-modifying enzymes and their cofactors. Identifying the cis elements that regulate epigenomic modification is critical for understanding the regulatory mechanisms that control gene expression patterns. We present Epigram, an analysis pipeline that predicts histone modification and DNA methylation patterns from DNA motifs. The identified cis elements represent interactions with the site-specific DNA-binding factors that establish and maintain epigenomic modifications. We cataloged the cis elements in embryonic stem cells and four derived lineages and found numerous motifs that have location preference, such as at the center of H3K27ac or at the edges of H3K4me3 and H3K9me3, which provides mechanistic insight about the shaping of the epigenome. The Epigram pipeline and predictive motifs are at <http://wanglab.ucsd.edu/star/epigram/>.

### Scientific Abstract:

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